

Appendix VI

Alignment of instant SEQ ID NO: 1 (nucleotides 770-1310) with SEQ ID NO: 1 of Sisk et al.

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Score =  994 bits (539),  Expect = 0.0
Identities = 540/541 (99%), Gaps = 0/541 (0%)
Strand=Plus/Plus

Query  770  GCCAAGAGTGAAGTACCGCTATAGAGTCATAAGGCCACCCCTGGCTCTTAT  829
|||||||G|||C|||A|||G|||A|||G|||T|||G|||A|||G|||T|||A|||C|||A|||G|||T|||A|||T
Sbjct  713  GCCAAGAGTGAAGTACCGCTATAGAGTCATAAGGCCACCCCTGGCTCTTAT  772
|||||||G|||C|||A|||G|||A|||G|||T|||G|||A|||G|||T|||A|||C|||A|||G|||T|||A|||T
Query  830  GCATGCCTATACGTGTTTGGCTTGGGCTATACACCCCGCTCCATGTTATAGGTG  889
|||||||G|||C|||A|||G|||C|||T|||A|||C|||G|||C|||T|||G|||T|||G|||T|||G|||T|||A|||T
Sbjct  773  GCATGCCTATACGTGTTTGGCTTGGGCTATACACCCCGCTCCATGTTATAGGTG  832
|||||||G|||C|||A|||G|||C|||T|||A|||C|||G|||C|||T|||G|||T|||G|||T|||G|||T|||A|||T
Query  890  ATGGTATACTAGCTATAGGTGTTGGGTATGACCATTAATGACCAACTCCCTATG  949
|||||||A|||T|||G|||G|||T|||A|||C|||T|||A|||G|||G|||T|||G|||T|||G|||T|||A|||T
Sbjct  833  ATGGTATACTAGCTATAGGTGTTGGGTATGACCATTAATGACCAACTCCCTATG  892
|||||||A|||T|||G|||G|||T|||A|||C|||T|||A|||G|||G|||T|||G|||T|||G|||T|||A|||T
Query  950  TGACGATACTTTCATTACTATCCATAACATGGCTTTCACACAACTCTCTTTATTG  1009
|||||||T|||G|||A|||C|||T|||T|||T|||C|||A|||T|||A|||C|||T|||G|||C|||T|||T|||T|||A|||T
Sbjct  893  TGACGATACTTTCATTACTATCCATAACATGGCTTTCACACAACTCTCTTTATTG  952
|||||||T|||G|||A|||C|||T|||T|||T|||C|||A|||T|||A|||C|||T|||G|||C|||T|||T|||T|||A|||T
Query  1010 CTATATGCCAACACACTGTCCTTCAGAGACTGACACGGACTCTGTATTTAACAGGA  1069
|||||||C|||T|||A|||T|||A|||G|||C|||C|||A|||A|||C|||A|||C|||G|||C|||T|||T|||T|||A|||T
Sbjct  953  CTATATGCCAACACACTGTCCTTCAGAGACTGACACGGACTCTGTATTTAACAGGA  1012
|||||||C|||T|||A|||T|||A|||G|||C|||C|||A|||A|||C|||A|||C|||G|||C|||T|||T|||T|||A|||T
Query  1070 GGTCTCATTTATATTACAAATTACATATACAACACACCCTCCCCAGTGCCCAGCT  1129
|||||||G|||G|||T|||C|||T|||C|||A|||T|||T|||A|||C|||A|||A|||T|||A|||C|||A|||C|||C|||G|||C|||A|||T
Sbjct  1013 GGTCTCATTTATATTACAAATTACATATACAACACACCCTCCCCAGTGCCCAGCT  1072
|||||||G|||G|||T|||C|||T|||C|||A|||T|||T|||A|||C|||A|||A|||T|||A|||C|||A|||C|||C|||G|||C|||A|||T
Query  1130 TTTTATTAAACATAACGTGGATCTCCACGGAAATCTCGGGTACGTGTTCCGGAAACGGTG  1189
|||||||T|||T|||T|||A|||A|||C|||A|||C|||G|||T|||G|||G|||A|||T|||C|||G|||G|||T|||A|||C|||G|||T
Sbjct  1073 TTTTATTAAACATAACGTGGATCTCCACGGAAATCTCGGGTACGTGTTCCGGAAACGGTG  1132
|||||||T|||T|||T|||A|||A|||C|||A|||C|||G|||T|||G|||G|||A|||T|||C|||G|||G|||T|||A|||C|||G|||T
Query  1190 GAGGGCAGTGTAGTCGTGAGCAGTACTCGTTGTCGCCGCGGCCACAGACATAATAGC  1249
|||||||G|||A|||G|||G|||C|||A|||G|||T|||G|||T|||A|||C|||G|||T|||G|||C|||G|||C|||A|||C|||A|||T|||A|||G|||C
Sbjct  1133 GAGGGCAGTGTAGTCGTGAGCAGTACTCGTTGTCGCCGCGGCCACAGACATAATAGC  1192
|||||||G|||A|||G|||G|||C|||A|||G|||T|||G|||T|||A|||C|||G|||T|||G|||C|||G|||C|||A|||C|||A|||T|||A|||G|||C
Query  1250 TGACAGACTAACAGACTGTTCCTTCCATGGCTTTCTGAGTCACCGCTTCAAC  1309
|||||||T|||G|||A|||C|||A|||G|||C|||T|||T|||C|||G|||G|||T|||T|||C|||G|||A|||T|||C|||A|||C|||C|||G|||T|||C|||A|||C
Sbjct  1193 TGACAGACTAACAGACTGTTCCTTCCATGGCTTTCTGAGTCACCGCTTCAAC  1252
|||||||T|||G|||A|||C|||A|||G|||C|||T|||T|||C|||G|||G|||T|||T|||C|||G|||A|||T|||C|||A|||C|||C|||G|||T|||C|||A|||C
Query  1310 G  1310
| 
Sbjct  1253 G  1253

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